

ECTA MAGG113

CTAF

ALLELE 1: 1 TTAAAGGGATATGTTTTTTCACTAATG-CEGTAAAAAATTCACCC--AgATTTTTCGCAATTTcttcttgaaaaaatgt
|||||
ALLELE 2: 1 TTAAGGGATATGTTTTTTCACTAATGc-GTAAAAAATTCACCCcaA-ATTTTTCGCAATTT-----

CTAR

ALLELE 1: 74
tagatataTCATGTTTTTTTACAAGCATTACAATAATATTCACTCGTATATTAGGAATTC 133
|||||

ALLELE 2: 61
-----ATCATGTTTTTTTACAAGCATTACAATAATATTCACTCGTATATTAGGAATTC 113

ECCMAAC405

A2D8F

ALLELE1: 1 TTTAAACCTTGGGTGATCGGGTATTACAGTACGAGGCCA-----ATCAACTAAATA-TCTGCA
|||||
ALLELE2: 1 TTTAAACCTTGGGTGATCGGGTATTACAGTACGAGGCCAATCAACTAAATAAT-TGCA

A2D8R

ALLELE1: 62 AACGATAATATAATTATAAGAAAAAGAC-aCACTTTGAGGGCATTTTTTGACTTGAGAGAACTCAGGTATCAATCTAA
|||||
ALLELE2: 74 AACGATAATATAATTATAAGAAAAAGACT-CACTTTGAGGGCATTTTTTGACTTGAGAGAACTCAGGTATCAATCTAA

MICROSATELLITE

ALLELE1: 138 AAGCAACGCTGTTCACTTGAGCTGAAACACCTGGAGGAGAAAGCAAAGCAAACCAACCGCAGACAGAGAAATAAAG
|||
ALLELE2: 150 AAGCAACGCTGTTCACTTGAGCTGAAACACCTGGAGGAGAAAGCAAAGCAAACCAACCGCAGACAGAGAAATAAAG

ALLELE1: 214 AACGGAACagagAGAGAGAGGAGGACCTTGTTCAAAGCAACGGGGACAACTTTAGAGCCCTGGCGCGCGTGGG
 |||||
ALLELE2: 226 AACGGAAC----AGAGAGAGAGGAGGACCTTGTTCAAAGCAACGGGGACAACTTTAGAGCCCTGGCGCGCGTGGG

ALLELE1: 291 GGTC AATAAGCGTAACCTGGCTGAGGACAGCCTCGGCG-
tCGTCCTTGCTGAAGCAGAAGAGGAAAGAG-CaCGAGA
|||||
ALLELE2: 299 GGTC AATAAGCGTAACCTGGCTGAGGACAGCCTCGGCGc-
CGTCCTTGCTGAAGCAGAAGAGGAAAGAGcC-CGAGA

ALLELE1: 365 CCAAGAGAACTCCTCGGAAGCAACGGGAATTC 397

ALLELE2: 373 CCAAGAGAAACTCTCGGAGCAACGGGAATTC 405

1875

E_{CG}M_{AGA}116
 ALLELE 1: 1 GAATTCGGTTATCTCAGACAACCTTTGTTGGTTTATAGTAAAGACACGATTAT
 ALLELE 2: 1 GAATTCGGTTATCTCAGACAACCTTTGTTGGTTTATAGTAAAGACACGATTAT

 ALLELE 1: 60 CCAGGCTTTGAGAGGCATAGAAATAATTTTTTATATAAATAAAAGTCTCTTTAA
 ALLELE 2: 60 CCAGGCTTTGAGAGGCATAGAAATAATTTTTTATATAAATAAAAGTCTCTTTAA

E_{ATG}M_{CGA}87
 Allele 1: 1 GAATTCATGGTTCTCTTAT-----GACATTGTTGCCAAGTAATACTACTATATAAAATTCAGATTGGGTTT
 Allele 2: 1 GAATTCATGGTTCTCTTATcttatGACATTGTTGCCAAGTAATACTACTATATAAAATTCAGATTGGGTTT

 Allele 1: 68 CTGATRAACCGTGGTCGTAA 87
 Allele 2: 73 CAGATRAACCGTGGTCGTAA 92

E_{CC}M_{ATG}161
 ALLELE1: 1 TTAAATGAAAATCGATCAAAATCAAAATATATATGCTTTTTTAGTTG-GGTTCAAGT-ACT
 ALLELE2: 1 TTAAATGAAAATCGATCAAAATCAAAATATATATGCTTTTTTTAGTTGt-GTTCAAGTtACT

 ALLELE1: 61 TTTTATTGAAAAATCGACCCAAAGTTGAAAACACATGTTTGAGAAATGTTTGT 116
 ALLELE2: 62 TTTTATTGAAAAATCGACCCAAAGTTGAAAACACATGTTTGAGAAATGTTTGT 117

 ALLELE1: 117 GCATCCAACGTTTTCTTGTACAATCAGCTGTGAGAGGGGAATTC 161
 ALLELE2: 118 GCATCCAACGTTTTCTTGTACAATCAGCTGTGAGAGGGGAATTC 162

E_{CC}M_{AG}114
 ALLELE1: 1 GAATTCACAGC-AGATTGTATCAAAATGATGTCCACAAAATGTTCAAGCATCTTA 59
 ALLELE2: 1 GAATTCACAG-CTAGATTGTATCAAAATGATGTCCACAAAATGTTCAAGCATCTTA 59

 ALLELE1: 60 GGGAACTGCTATTCTTACTTAAATTTTTTATGACATCCAAAGTGTGCTTTAA 114
 ALLELE2: 60 GGGAACTGCTATTCTTACTTAAATTTTTTATGACATCCAAAGTGTGCTTTAA 114

FIG. 1a-2

E_{ATG}M_{CGA}87 BAC extension and TaqMan probe and primers

Allele 1:	ttatcatccaaaattaaaattgaaaaactttaatacaaaatgcacatttttgaggccattcatgtc 	
Allele 2:	ttatcatccaaaattaaaattgaaaaactttaatacaaaatgcacatttttgaggccattcatgtc 	<u>TMA5F</u>
Allele 1:	atctcttggctcgagtccttatcattctgtggattgaattcattgggttctctttat-----GACATTGTT 	<u>TMA5-RE</u>
Allele 2:	atctcttggctcgagtccttatcattctgtggattgaattcattgggttctctttatGACATTGTT 	<u>TMA5R</u>
Allele 1:	GCCAAGTAATACTACTATATAAAATTCAGATTGGGTTTCTGATAACCGTGGTCGTTAACTactatataatacc 	<u>TMA5-S</u>
Allele 2:	GCCAAGTAATACTACTATATAAAATTCAGATTGGGTTTCTGATAACCGTGGTCGTTAACTactatataatacc 	<u>ATG4BACF</u>

FIG. 1b

BEST AVAILABLE COPY

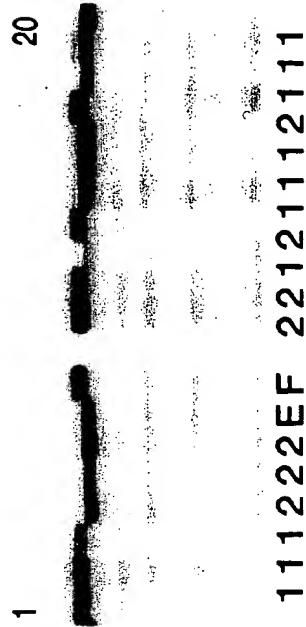


FIG. 2B



FIG. 2A

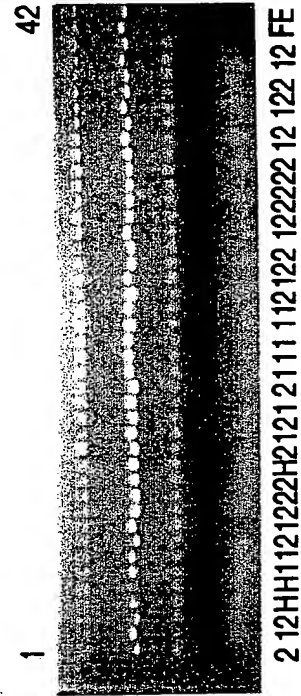


FIG. 2D

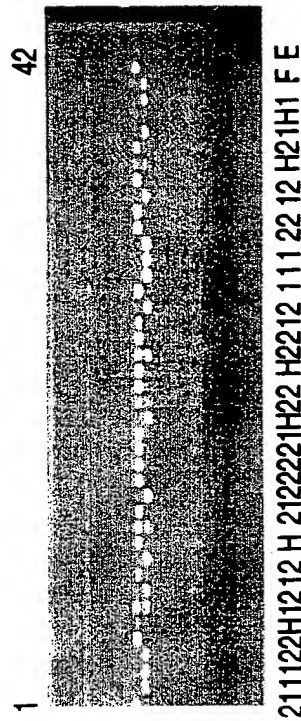


FIG. 2C

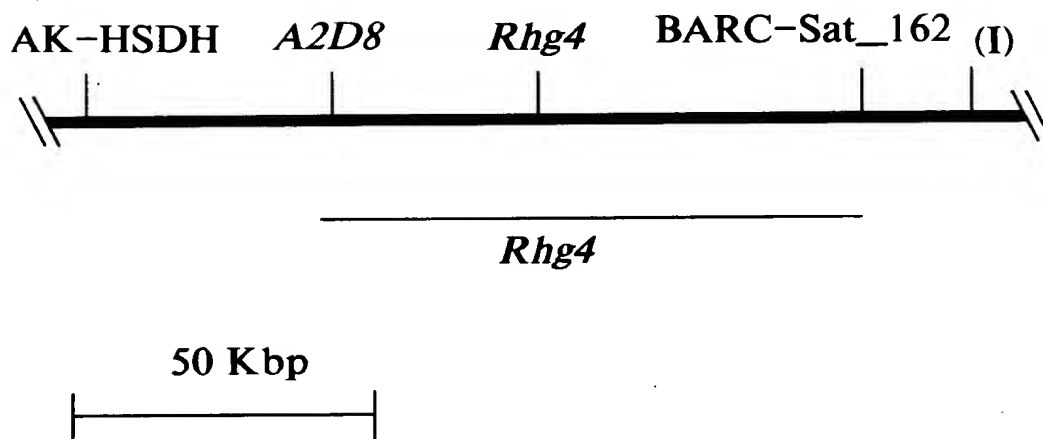


FIG. 3

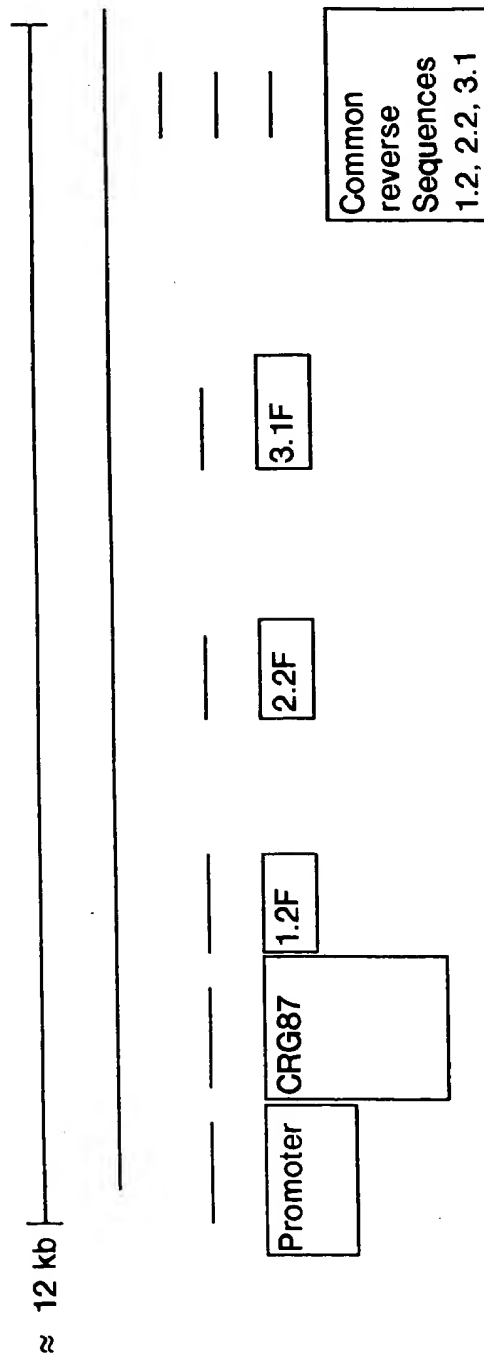


FIG. 4

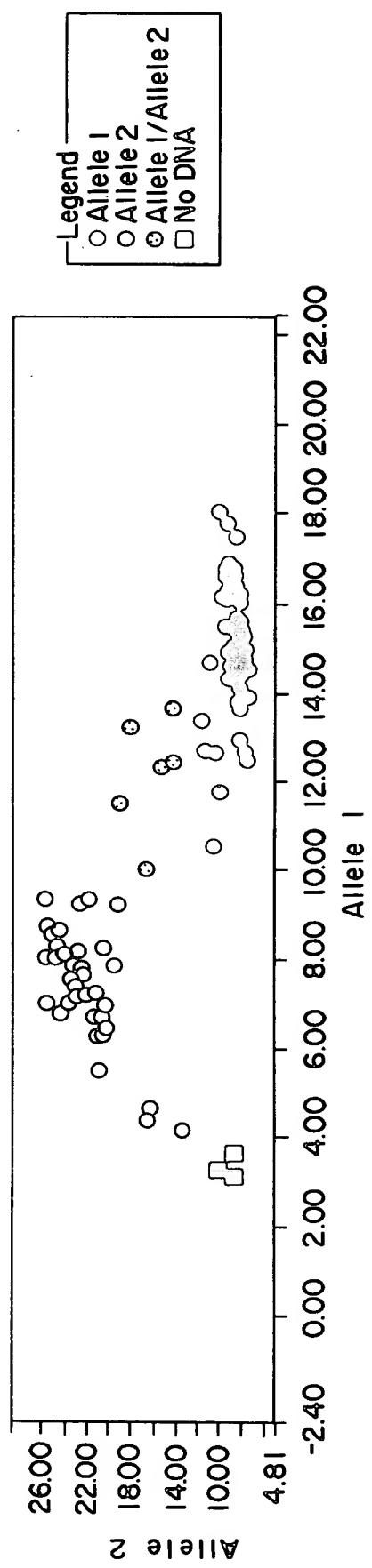


FIG. 5A

	1	2	3	4	5	6	7	8	9	10	11	12
A	2	1	1 and 2	1	1	1	1	1	1	2	1	2
B	1	2	2	1	1 and 2	2	2	1	2	1 and 2	1	2
C	1	2	1	1	1	2	2	1	1	1	1	2
D	1	1	2	1	2	2	2	1 and 2	2	1	1	2
E	1	1 and 2	2	2	2	No Amp	2	1	1	1	1	2
F	1 and 2	1	2	2	1	1	2	2	2	2	1	2
G	1	1	1	2	1	2	2	1	1	1	1	2
H	2	2	2	2	1	1	2	1	1	1	No Amp	No Amp

FIG. 5B



BEST AVAILABLE COPY

FIG. 6A

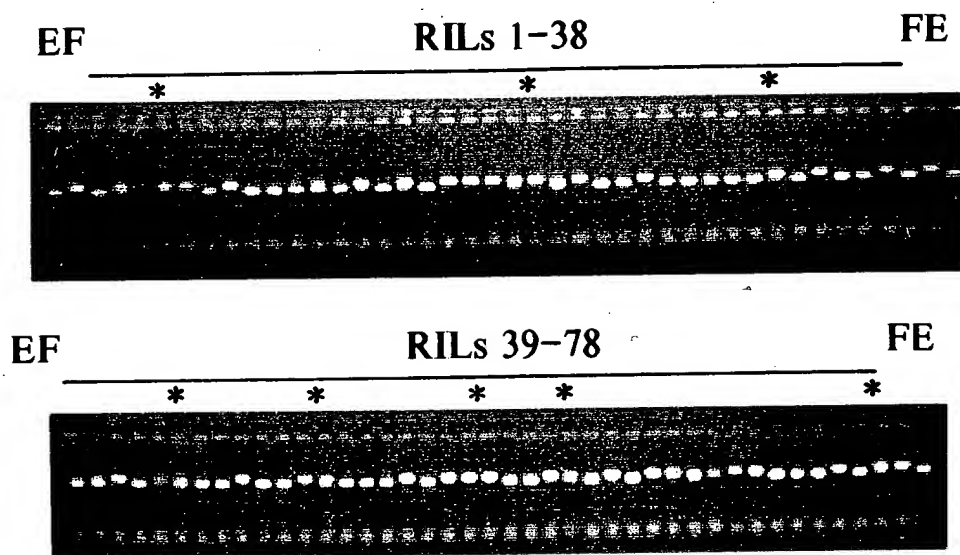


FIG. 6B

Synthetic rhg1 gene

1
AATGGGAGGAGTGGGAAAGACAGTGGCTATGGAGCTTGTTCCGGAGGTTGGGTTGGAAT
CAAGTGTGCTCAGGGACAGGTTATTGTGATCCAGCTTCCTTGGAAGGGTTTGAGGGGTC
GAATCACCGACAAAATTGGCCAACTTCAAGGCCTCAGGAAGCTTAGTCTTCATGATAAC
CAAATTGGTGGTTCAATCCCTTCAACTTTGGGACTTCTTCCCAACCTTAGAGGGGTTCA
GTTATTCAACAATAGGCTTACAGGTTCCATACCTCTTTCTTTAGGTTTCTGCCTTTGCT
TCAAGTCTCTTGACCTCAGCAACAACCTTGCTCACAGGAGCAATCCCTTATAGTCTTGCT
AATTCCACTAAGCTTTATTGGCTTAACTTGAGTTTCAACTCCTTCTCTGGTCCTTTACC
AGCTAGCCTAACTCACTCATTTTCTCTCACTTTTCTTTCTCTTCAAATAACAATCTTT
CTGGCTCCCTTCCTAACTCTTGGGGTGGGAATTCCAAGAATGGCTTCTTTAGGCTTCAA
AATTTGATCCTAGATCATAACTTTTTCACTGGTGACGTTCTTGCTTCTTTGGGTAGCTT
AAGAGAGCTCAATGAGATTTCCCTTAGTCATAATAAGTTTAGTGGAGCTATAACCAAATG
AAATAGGAACCTTTCTAGGCTTAAGACACTTGACATTTCTAATAATGCCTTGAATGGG
AACTTGCCTGCTACCCTCTCTAATTTATCCTCACTTACACTGCTGAATGCAGAGAACAA
CCTCCTTGACAATCAAATCCCTCAAAGTTTAGGTAGATTGCGTAATCTTTCTGTTCTGA
TTTTGAGTAGAAACCAATTTAGTGGACATATTCCTTCAAGCATTGCAAACATTTCTCTCG
CTTAGGCAGCTTGATTTGTCACTGAATAATTTCACTGGAGAAATTCCAGTCTCCTTTGA
CAGTCAGCGCAGTCTAAATCTCTTCAATGTTTCTTACAATAGCCTCTCAGGTTCTGTCC
CCCCCTGTGCTTGCCAAGAAATTTAACTCAAGCTCATTTGTGGGAAATATTCAACTATGT
GGGTACAGCCCTTCAACCCCATGTCTTTCCCAAGCTCCATCACAAGGAGTCATTGCCCC
ACCTCCTGAAGTGTCAAACATCACCATCATAGGAAGCTAAGCACCAAAGACATAATTC
TCATAGTAGCAGGAGTTCTCCTCGTAGTCCTGATTATACTTTGTTGTGTCTGCTTTTC
TGCCTGATCAGAAAGAGATCAACATCTAGGCCGGGAACGGCCAAGCCACCCGAGGGTAG
AGCGGCCACTATGAGGACAGAAAAAGGAGTCCCTCCAGTTGCTGGTGGTGATGTTGAAG
CAGGTGGGGAGGCTGGAGGGAACTAGTCCATTTTGATGGACCAATGGCTTTTACAGCT
GATGATCTCTTGTGTGCAACAGCTGAGATCATGGGAAAGAGCACCTATGGAAGTGTTA
TAAGGCTATTTTGGAGGATGGAAGTCAAGTTGCAGTAAAGAGATTGAGGGAAAAGATCA
CTAAAGGTCATAGAGAATTTGAATCAGAAGTCAGTGTTCTAGGAAAAATTAGACACCCC
AATGTTTTGGCTCTGAGGGCCTATTACTTGGGACCCAAAGGGGAAAAGCTTCTGGGTTT
TGATACATGTCTAAAGGAAGTCTTGCTTCTTTCCTACATGGAAGGTTTCGTGTGCTGGTT
CTTTCATTAAAGTGTTGTGTGTGCTGGTCTTTAATTATAATTTGGAGTTTACCTTAGT
AATCTGTATAATTCTAATCGGAGAACAGTACAAACAAAAACACCTAAGGAACAACACCT
TANCTTTAATATACCATATCAATAAAGTGAAATATTTTCTTGGTCATCTTGATGCAGGG
GGAAGTGAACATTCATTATTGGCCACAAGATTAATAATAGCCCAAGCCTTGGCCCGGGCT
TGTTTGCCTTCATTCCCAGGAGAACATCATACATGGGACCTCNCATCCAGCAATGTGTG
GCTTGATGAAAAACAAATGCTAAATTCAGATTTTGGTCTTTTTTCGGGTGATGTCAAC
TGCTGCTAATTCCAACGTGATAGCTACAGCTGGAGCATTGGATACCGGGCACCTGAGCT
CTCAAAGCTCAAGAAAGCAAACACTAAAAGTATCTACAGTCTTGGTGTTATCTTGT
TAGAACTCCTAACGAGGAAATCACCTGGGGTGTCTATGAATGGACTAGATTTGCCTCAG
TGGGTTGCCTCAGTTGTCAAAGAGGAGTGGACAAATGAGGTTTTTGATGCAGACTTGAT
GAGAGATGCATCCACAGTTGGCGACGAGTTGCTAAACACGTTGAAGCTCGCTTTGCACT
GTGTTGATCCTTCTCCATCAGCAGCAGCAGGAAGTTCATCAAGTTCTCCAGCAGCTGAAG
AGATTAGACCAGAGAGATCAGTCACAGCCAGTCCCGGGGACGATATCGTATAGCACAAA
TTTTGCATTGATTTTTTTTGTGCCAAATGTAGTAGGCCTACTATATATATGTTCTATGAT

FIG. 7A

TCTTTCATTCTTATATTATTTTTGCCTGTTTGAATGCTTGAATTTGTACATACTCATAC
TACAATAAGGTGTAGTTCTGGTTAATTTTACCTCTACCTCAAAGCTGGGGTGTAAATTCT
GTTTCCTCCAAGGCACATAATAGTTGAAAATAGTTCTCAGGAGCATTCAATTGTTTATTC
TGCAAGATTCTCTTTTACGGCTGCTATCTTCTATGCATGCCCTGCCCATAAATGCATTA
TGAAGAATTGTAACGGCTGTGTTTTTGGACTTCTTCAAAAAGTTTATGTTATTGCCAGG
TGTATATATCAACATGTTTTTAAAGATTTTCAAACAATCAGGTTTTAGATGTGGGTTTGC
ATGCATGAGATTGGACTAGTGCGCTTGATGTAGTATAAAATATAAATTGTCCAATCAAG
CACCTCTACATGTCCAAATAATGGGCCTTATGAACTTAATTTTTTAAATTACAACTA
CAGTAATCTTTTTGAATAAAGATTTACAAATTACAACNGACATGTGAAGCNGCATCTTT
NATTGNCAATCTTTCAAGTTACTCTATTATTTTCTGCN

3105bp

FIG. 7B

Rhg1 Peptide

NGRSGKDSGYGACSGGWVGIKCAQGQVIVIQLPWKGLRGRIT
DKIGQLQGLRKLSLHDNQIGGSIPSTLGLLPNLRGVQLFNNRLG
SIP

LSLGFCPLLQSLDLSNNLLTGAIP
YSLANSTKLYWLNLSFNFSGPLP
ASLTHSFSLTFLSLQNNNLSGSLPNSWGG
NSKNGFFRLQNLILDHNFFTGDVP
ASLGSLRELNEISLSHNKFSGAIP
NEIGTLSRLKTLDISNNALNGNLP
ATLSNLSSLTLLNAENNLLDNQIP
QSLGRLRNLSVLILSRNQFSGHIP
SSIANISSLRQLDLSLNNFSGEIP
VSFDSQRSLNLSNVSYNSLSGSVP

PLLAKKFNSSSFVGNIQLCGYSP
STPCLSQ

APSQGVIAAPPPEVSKHHHR

KLSTKDIILIVAGVLLVVLIIILCCVLLFCLIRKRS

TSKAGNGQATEGRAATMRTEKGVPPVAGGDVEAGGEAGGKLVHF
DGPMAFTADDLLCATAEIMGKSTYGTVYKAILEDGSQVAVKRLR
EKITKGHREFESEVSVLGKIRHPNGLALRAYYLGPKEKLLVFD
YMSKGGLLLFYMEGSCAGSFIKVLCLVFNYNLEFYLSNLYNSN
RRTVQTKTPKEQHLXFNIPYQ

-SEIFSWSS-CRGN-TFIIGHKMKIXQDLAVACSPSPFETSMD
LXSSNV CX-NXMLKLQFWSFSVDVNCC-FQRDSYSWSIGIPGT-
ALKAQESKH-N-YLQSWCYLVRTPNEEITWGVYEWTRFASVGCL
SCQRGVDK-GF-CRLDERCIHSWRRVAKHVEARFALC-SFSIS
TTRSSSSSPAAGRD-TREISHSQSHLPGRPLEPYSESY

FIG. 7C

Score E
(bits) Value

Sequences producing significant alignments:

pir:T46070	hypothetical protein T18N14.120 - Arabidopsis thaliana	632	e-180
pir:T47727	hypothetical protein F18O21.60 - Arabidopsis thaliana	344	1e-95
pir:T04587	hypothetical protein F23E13.70 - Arabidopsis thaliana	268	9e-71
pir:T49038	hypothetical protein T5P19.20 - Arabidopsis thaliana	257	2e-67
pir:T48210	hypothetical protein T20L15.160 - Arabidopsis thaliana	241	1e-62
pir:T05050	protein kinase homolog M3E9.30 - Arabidopsis thaliana	238	2e-61
pir:T18536	receptor-like protein kinase - Ipomoea nil (Japanese...	236	3e-61
pir:T48489	receptor-like protein kinase - Arabidopsis thaliana	236	5e-61
pir:T10515	disease resistance protein Cf-2.2 - currant tomato	235	6e-61
pir:T10504	disease resistance protein Cf-2.1 - currant tomato	235	6e-61
pir:T30553	disease resistance protein Hcr2-5D - tomato	229	4e-59
pir:S27756	receptor-like protein kinase 5 (EC 2.7.1.-) precursor...	227	1e-58
pir:T48499	receptor-like protein kinase-like protein - Arabidop...	226	3e-58
pir:T46033	receptor protein kinase-like protein - Arabidopsis t...	226	4e-58
pir:T05335	hypothetical protein F1C12.190 - Arabidopsis thaliana	221	1e-56
pir:T10636	hypothetical protein T13K14.100 - Arabidopsis thaliana	219	7e-56
pir:T05898	hypothetical protein F6H11.170 - Arabidopsis thaliana	218	1e-55
pir:T45717	receptor-kinase like protein - Arabidopsis thaliana	212	7e-54
pir:T05322	hypothetical protein F18F4.240 - Arabidopsis thaliana	211	1e-53
pir:T10659	probable serine/threonine-specific protein kinase (E...	211	2e-53
pir:T03784	probable receptor protein kinase - rice	208	1e-52
pir:T50851	receptor protein kinase homolog [imported] - soybean	201	1e-50
pir:T45647	receptor protein kinase-like protein - Arabidopsis t...	199	5e-50
pir:T45718	receptor-kinase like protein - Arabidopsis thaliana	199	7e-50
pir:T50850	receptor protein kinase homolog [imported] - soybean	199	7e-50
pir:T45645	receptor kinase-like protein - Arabidopsis thaliana	196	3e-49
pir:T09356	brassinosteroid-insensitive protein BRI1 - Arabidops...	196	3e-49
pir:T00712	protein kinase homolog F22O13.7 - Arabidopsis thaliana	190	2e-47
pir:A57676	protein kinase Xa21 (EC 2.7.1.-), receptor type prec...	190	3e-47
pir:S39476	kinase-like transmembrane protein TMKL1 precursor - ...	188	1e-46
pir:T02154	protein kinase homolog T1F15.2 - Arabidopsis thaliana	188	1e-46
pir:T10725	protein kinase Xa21 (EC 2.7.1.-) A1, receptor type - ...	186	5e-46
pir:T05897	protein kinase homolog F6H11.160 - Arabidopsis thaliana	184	1e-45
pir:T04313	protein kinase Xa21 (EC 2.7.1.-), receptor type - rice	183	3e-45
pir:T10727	protein kinase Xa21 (EC 2.7.1.-) D, receptor type - ...	181	2e-44

FIG. 7D

>pir:T46070 hypothetical protein T18N14.120 - Arabidopsis thaliana
Length = 836

Score = 632 bits (1613), Expect = e-180
Identities = 329/550 (59%), Positives = 400/550 (71%), Gaps = 2/550 (0%)
Frame = +1

Query: 7 RSGKDSGYGACSGGWVGKCAQGVIVIQLPWKGLRGRITDKIGQLQGLRKLSDLHDNQIG 186
+S +S GW GIKC +GQV+ IQLPWKGL G I++KIGQL LRKLSLH+N I
Sbjct: 72 KSWNNSASSQVCSGWAGIKCLRGQVVAIQLPWKGLGGTISEKIGQLGSLRKLSDLHNNVIA 131

Query: 187 GSIPSTLGLLPNLRGVQLFNNRLTGSIPLSLGFCLCFKSLDLSNNLLTGAIPYSLANSTK 366
GS+P +LG L +LRGV LFNNRL+GSIP+SLG C ++LDLS+N LTGAIP SL ST+
Sbjct: 132 GSVPRSLGYLKSRLRGVYLFNNRLSGSIPVSLGNCPLLQNLDLSSNQLTGAIPPSLTESTR 191

Query: 367 LYWLNLFSNFSGGLPASLTHSFSLSLTLQNNNLSGSLPNSWGGNSKNGFFRLQNLILD 546
LY LNLFSNFS SGPLP S+ S++LTFL LQ+NNLSGS+P+ + NG L+ L LD
Sbjct: 192 LYRLNLFSNLSGGLPVSVARSYTLTFLDLQHNNLSGSIPDFF---VNGSHPLKTLNLD 247

Query: 547 HNFFTGDVPASLGSRLRELNEISLSHNKFSGAIPNEIGTSLRKLTLDISNNALNGNLPATL 726
HN F+G VP SL L E+S+SHN+ SG+IP E G L L++LD S N++NG +P +
Sbjct: 248 HNRFGAVPVSLCKHSLLEEVSISHNQLSGSIPRECGGLPHLQSLDFSYSNSINGTIPDSF 307

Query: 727 SNLSSLTLLNAENLLDNQIPQSLGRLRNLSVLILSRNQFSGHIPSSIANISSLRQLDLS 906
SNLSSL LN E+N L IP ++ RL NL+ L L RN+ +G IP +I NIS +++LDLS
Sbjct: 308 SNLSSLVSLNLESNHLKGPIPAIDRLHNLTELNLKRKNKINGPIPETIGNISGIKKLDLS 367

Query: 907 LNNFSGEIPVSFDSQSRSLNLFNVSYNSLSGSVPPLAKKFNSSSFVGNQLCGYSPSTPC 1086
NNF+G IP+S L+ FNVSYN+LSG VPP+L+KKFNSSSF+GNIQLCGYS S PC
Sbjct: 368 ENNFTGPIPLSLVHLAKLSSFNVSYNTLSGPVPPVLSKKFNSSSFVGNQLCGYSSSNPC 427

Query: 1087 LSQAPSQGVIAAPP--PEVSKHHHHRKLSTKDIILIVAGVLLVLIILCCVLLFCLIRKRS 1260
+ + P + + HHRKLS KD+ILI G LL +L++LCC+LL CLI+KR+
Sbjct: 428 PAPDHHHPLTSLPTSSQEPRKHHRKLSVKDVLIAIGALLAILLLLCCILLCCLIKKRA 487

Query: 1261 TSRPGTAKPPEGRAATMRTEKGVPPVAGGDVEAGGEAGGKLVHFDGPMFTADDLLCATA 1440
K +G+ T +EK V G AGGE GGKLVHFDGP FTADDLLCATA
Sbjct: 488 -----ALKQKDGKDKT--SEKTVSAGVAGTASAGGEMGGKLVHFDGPFVFTADDLLCATA 540

Query: 1441 EIMGKSTYGTVYKAILEDGSQVAVKRLREKITKGHREFESEVSVLGKIRHPNVLALRAYY 1620
EIMGKSTYGT YKA LEDG++VAVKRLREK TKG +EFE EV+ LGKIRH N+LALRAYY
Sbjct: 541 EIMGKSTYGTAYKATLEDGNEVAVKRLREKTTKGVKEFEGETALGKIRHQNLALRAYY 600

Query: 1621 LGPKGEKLLGFD 1656
LGPKGEKLL FD
Sbjct: 601 LGPKGEKLLVFD 612

FIG. 7E

Score = 185 bits (464), Expect = 1e-45
Identities = 93/161 (57%), Positives = 122/161 (75%), Gaps = 3/161 (1%)
Frame = +2

Query: 1943 GLVCLHSQENIIHGTSHPAMCGLMKKNC*NS---DFGLFRVDVNCC*FQRDSYSWSIGYR 2113
GL LHS EN+IH + ++ ++ N+ D+GL R+ + + ++GYR
Sbjct: 647 GLAHLHSNENMIH--ENLTASNILLDEQTNNAHIADYGLSRLMTAAAATNVIATAGTLGYR 704

Query: 2114 APELSKLKKANTKTDIYSLGVILLELLTRKSPGVSMNGLDLPQWVASVVKEEWTNEVFDA 2293
APE SK+K A+ KTD+YSLG+I+LELLT KSPG NG+DLPQWVAS+VKEEWTNEVFD
Sbjct: 705 APEFSKIKNASAKTDVYSLGIIILELLTGKSPGEPTNGMDLPQWVASIVKEEWTNEVF DL 764

Query: 2294 DLMRDASTVGDELLNTLKLALHCVDPSPSARPEVHQVLQQLKRL 2425
+LMR+ +VGDELLNTLKLALHCVDPS+ARPE +QV++QL+ +
Sbjct: 765 ELMRETQSVGDELLNTLKLALHCVDPSAARPEANQVVEQLEEI 808

FIG. 7F